

SEQUENCE LISTING

<110> Huston, James S.  
Wils, Pierre  
Zhu, Quan  
Laurent, Olivier  
Marasco, Wayne A.  
Scherman, Daniel

<120> BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID  
DELIVERY

<130> 23611-A USA

<140> As yet unassigned  
<141> 2001-06-25

<150> 60/213,653  
<151> 2000-06-23

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<170> PatentIn Ver. 2.0

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<400> 37

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tcctgtaaagg ttctcgata cagttttacc agctactgga tgcgcgggtt gcgcaggatc 120  
ccgggaaag gcctggatca catggggctc atctatcctg tgactctga caccaaatac 180  
agccgtctc tccaaggcca ggtcaccatc tcagtcgaca agtccgtcag cactgcctac 240  
ttgcaatggc gcagttgttgc gcccctcgac agcgcgtgtt atttttgtgc gagacatgac 300  
gtggatatttgcgttgc caactggcga aagtggcttg aatacttcca gcattgggc 360  
caggcacccttggtcacccgtt ctcctcgatggggcggtt cagggcgagg tggtctggc 420  
gggtgcggat cgcagtctgtt gttgacgcag cccgcctcgt tgctcgcccccaggacag 480  
aaggtcacca ttcctgttc tggaaaggcgc tccaacatttggaaataattatgtatccctgg 540  
taccaggcaggcccccaggaa agccccccaaatcttcatctt atgatcacac caatcgccc 600  
gcagggttcccttcggatt ctctggccta aagtggcgcctcgcctcgcctcgcctc 660  
agtgggttcccttcggaggatggggatgatctgttattactgttcttcctggatcatacccttc 720  
tcgggctgggttggggggaggaaacaaatggacgcgttccatggcgcgcacacat 780  
cataccatc acgggtgttgc cgggtgc 807

<210> 38

<211> 282

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Human/murine  
chimeric single chain binding polypeptide  
(C6ML-3-9sFv'-L1-KDEL)

<400> 38

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met  
35 40 45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys  
85 90 95

Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp

100 105 110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
115 120 125

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser  
130 135 140

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln  
145 150 155 160

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn  
165 170 175

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu  
180 185 190

Ile Tyr Asp His Thr Asn Arg Pro Ala Gly Val Pro Asp Arg Phe Ser  
195 200 205

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Phe Arg  
210 215 220

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Tyr Thr Leu  
225 230 235 240

Ser Gly Trp Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Ala  
245 250 255

Ala Ala His His His His Gly Gly Gly Cys Leu Glu Ser  
260 265 270

Ser Ser Ser Gly Ser Glu Lys Asp Glu Leu  
275 280

<210> 39  
<211> 846  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Human/murine  
chimeric single chain binding polypeptide  
(C6ML-3-9sFv'-L1-KDEL)

<400> 39  
caggtgcagc tggtgccagtc tggggcagag gtgaaaaagc ccggggagtc tctgaagatc 60

tcctgtttaagg gttctggata cagcttacc agctactgga tcgcctgggt gcgcaggatg 120  
cccgaaaaag gcttggagta catggggctc atctatctgt gtgactctga caccataatc 180  
agccgttctt tccaaggccca ggttaccatc tcagtcgaca agtccctcgact cactgcctac 240  
tttcaatggaa gcatgttgcgaa gcccggcgtt atttttgtgc gagacatgac 300  
gtggatatt gcatgttgcgaa aacttcgca aagtggccctg aataacttcca gcatggggc 360  
caggccaccc tggtcacgtt ctcttcagggtt ggaggccgtt caggccggagg tggtctggc 420  
ggtggcgat cgcaggatgtt gtttgcgac cggccctcgact tgcgttggc cccaggacac 480  
aaggtaacca tcttcgttgcgaa tggaagcagc tccaaacattt ggaataatattt tgatctgg 540  
taccagcgc tcccaaggaaac agcccccaaa ctccctcatct atgatcacac caatcgcc 600  
gcagggggtcc ctgaccgatt ctctggcttca aagtctggc cctcagccctt cttggccatc 660  
agtgggttcc ggttccggaga tgaggctgtat tattactgtt ctccctggaa ctacaccc 720  
tcgggctggg tggtcgggg aggaaccaa ctgaccgttcc taggttggc cgcacacat 780  
catcaccatc acgggtgggg cggctgcctc gagtcctcta gctctggatc cgaaaaagat 840  
gaactg 846

<210> 40

<211> 287

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human/murine  
chimeric single chain binding polypeptide  
(C6ML3-9sFv'-L2-KDEL)

<400> 40

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met  
35 40 45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys  
85 90 95

Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp  
100 105 110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser

115	120	125
Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser		
130	135	140
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln		
145	150	155
Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Asn Ile Gly Asn Asn		
165	170	175
Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu		
180	185	190
Ile Tyr Asp His Thr Asn Arg Pro Ala Gly Val Pro Asp Arg Phe Ser		
195	200	205
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Phe Arg		
210	215	220
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Tyr Thr Leu		
225	230	235
240		
Ser Gly Trp Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Ala		
245	250	255
260	265	270
Ala Ala His His His His His Gly Gly Gly Gly Cys Leu Glu Ser		
Ser Ser Ser Gly Ser Ser Ser Gly Ser Glu Lys Asp Glu Leu		
275	280	285

<210> 41

<211> 861

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Human/murine  
chimeric single chain binding polypeptide  
(C6ML3-9sFv'-L2-KDEL)

<400> 41

caggtgcagc tggtgcaagtc tggggcagag gtgaaaaagc ccggggagtc tctgaagatc 60  
tcctgttaagg gttctggata cagcttttacg agctactgga tcgcctgggt ggcggcagatg 120  
cccgggaaag gcctggagta catggggctc atctatcctg tgactctga caccaaatac 180  
agcccgctct tccaaggcca ggtcaccatc tcagtcgaca agtccgtcag cactgcctac 240

ttgcaatggaa gcagtctgaa gcccctcgac agcgcggcgtt atttttgtgc gagacatgac 300  
gtggatatt gcagtagttc caactgcgc aagtggcctg aatacttcca gcattgggc 360  
cagggcaccc tggtcacccgt ctccctcagg ggaggcgggtt caggcggagg tggctctggc 420  
ggtggcggat cgcaagtctgtt gttgacgcagc cggccctcag tgcgtcgcccccaggacag 480  
aaggtcacca tccctctgc tggaaaggcagc tccaaacatgg aataatttttgcgtcgcc 540  
taccagcagc tcccgagaaac agccccccaa ctcctcatct atgatcacac caatcgcccc 600  
gcagggttcc ctgaccggat ctctggctcc aagtctgcgc cttcgcctc cttggccatc 660  
agtgggttcc ggtccggagga tgaggctgtt tattactgtt cttctggga ctacaccctc 720  
tcggctggg tggtcggcgg aggaaaccaag ctgaccgttcc taggtcgccgc cgcacacccat 780  
catcaccatc acgggtgggg cggctgcctc gagtttagca gttccgggttcc ctcttagctt 840  
ggatccgaaa aagatgaact g 861

<210> 42

<211> 296

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human/murine  
chimeric single chain binding polypeptide  
(C6ML3-9sFv'-L2-H14)

<400> 42

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met  
35 40 45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys  
85 90 95

Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp  
100 105 110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
115 120 125

Ser Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser

100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400 420 440 460 480 500 520 540 560 580 600 620 640 660 680 700 720 740 760 780 800 820 840 860 880 900 920 940 960 980 1000

130	135	140
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln		
145	150	155
Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn		
165	170	175
Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu		
180	185	190
Ile Tyr Asp His Thr Asn Arg Pro Ala Gly Val Pro Asp Arg Phe Ser		
195	200	205
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Phe Arg		
210	215	220
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Tyr Thr Leu		
225	230	235
240		
Ser Gly Trp Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Ala		
245	250	255
Ala Ala His His His His His Gly Gly Gly Cys Leu Glu Ser		
260	265	270
Ser Ser Ser Gly Ser Ser Ser Gly Ser Lys Lys Ser Ala Lys Lys		
275	280	285
Thr Pro Lys Lys Ala Lys Lys Pro		
290	295	

<210> 43

<211> 888

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Human/murine  
chimeric single chain binding polypeptide  
(C6ML3-9sFv'-L2-H14)

<400> 43

caggtgcagc tgggtcagtc tggggcagag gtgaaaaagc cggggagtc tctgaagatc 60  
tcctgttaagg gtctcgata cagcttacc agctactgga tcggctgggt ggcggatgc 120  
ccgggaaag gcctggatc catggggctc atctatctgc tgactctga caccaaatac 180  
agcccgatcc tccaaaggcca ggtcaccatc tcagtcgaca agtccgtcag cactgcctac 240

ttgcaatgg agcgtctgaa gcccctggac agcggccgtgt atttttgtgc gagacatgac 300  
gtgggatatt gcagtagttt caactgcgc aagtggcttg aatacttcca gcattgggc 360  
cagggcacc tggtcacccgt ctcttcagggt ggaggccgtt caggccggagg tggctctgg 420  
ggtggccgtt cgcaatgtgt gttgacgcgc cggccctcg tgcgtcgccccc 480  
aagggtcacca tccctctgtc tggaaaggcgc tccaaacattt ggaataatggatctctgg 540  
taccagcagc tcccaaggaaac agcccccaaa ctccatctat atgatcacac caatcgcccc 600  
gcagggggtcc ctggccgtt cttctggccaa aagtctggca cttccatctt cttggccatc 660  
agtgggttcc gggtccggagg tgaggctgtat tattactgtg cttccctggga ctacaccctc 720  
tcggccgtgg tggtccggccgg aggaaaccaag ctgaccgtcc tagtgcggc cgcacacat 780  
catcaccatc acggctgtgg cggctgcctc gagtttagca gtcgggttc ctcttagctc 840  
ggatccaaga aaagcgcgaa aaagaccccg aagaaagcga agaaaaccg 888

<210> 44

<211> 291

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Human/murine  
chimeric single chain binding polypeptide  
(C6ML3-9sFv'-L2-nls)

<400> 44

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met  
35 40 45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys  
85 90 95

Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp  
100 105 110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
115 120 125

Ser Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser

130

135

140

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln  
 145 150 155 160

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn  
 165 170 175

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu  
 180 185 190

Ile Tyr Asp His Thr Asn Arg Pro Ala Gly Val Pro Asp Arg Phe Ser  
 195 200 205

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Phe Arg  
210 215 220

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Tyr Thr Leu  
 225 230 235 240

Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala  
 245 250 255

Ala Ala His His His His His Gly Gly Gly Gly Cys Leu Glu Ser  
260 265 270

Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser Thr Pro Pro Lys Lys Lys  
275 280 285

Arg Lys Val  
290

<210> 45  
<211> 873  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Human/murine  
chimeric single chain binding polypeptide  
(C6ML3-9sFv'-L2-nls)

```
<400> 45
cagggtcagtc tgggtcagtc tggggcagag gtgaaaaagc cggggagtc tctgaagatc 60
tcctgttaagg gttctggata cagtttacc agctactgga tcgcctgggt ggcgcagatc 120
ccggggaaag gcgttggagta catggggctc atctatctgt gtgactctga caccaaaaatc 180
agccccgtct tccaaaggcca ggtcaccatc tcaagtgcaca agtccgtcag cactgcctac 240
```

ttgcaatggaa gcagtctgaa gcccctcgac agegcgcgtgt atttttgtgc gagacatgac 300  
gtggatatt gcagtagttc caactgcgc aagtggcctg aatacttcca gcattgggc 360  
cagggcaccc tggcacccgt ctccctcagggt ggaggcggtt caggcgagg tggctctggc 420  
ggtggcgat cgcaagtctgt gttgacgcag ccgcgcctcg tgcgtcgcccccaggacag 480  
aaggtcacca ttcctgtcc tggaaacgc tccaaacattt ggaataattt tgatctctgg 540  
taccagcage tcccgaaac agccccaaat ctcctcatct atgatcacac caatcgcccc 600  
gcaggggtcc ctgaccgat ctctggctcc aagtctggca cttcagccctc cttggccatc 660  
agtgggtcc ggtccgagga tgaggctgat tattactgtg ctcctggga ctacaccctc 720  
tcgggtggg tggcggcgg aggaaaccaag ctgaccgatcc taggtcgccgc cgacacccat 780  
catcaccatc acgggtgtgg cggctgcctc gagtcttagca gtcgggttc ctctagctct 840  
ggatccactc cgccgaaaaa gaaacgtaaa gtg 873